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SEQUENCE LISTING

<110> SODE, Koji

<120> Glucose dehydrogenase beta-subunit and DNA encoding the same

<130> G780-OP1551

<141> 2003-04-25

<150> JP 2002-125353

<151> 2002-04-26

<160> 19

<170> PatentIn Ver. 2.0

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<211> 2467

<212> DNA

<213> Burkholderia cepacia

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<221> CDS

<222> (258)..(761)

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<221> CDS

<222> (764)..(2380)

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<222> (2386)..(2466)

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tacgaatggc tgacacattg aatggactat aaaaccattg tccgttccgg aatgtgcgcg 180
tacatttcag gtccgcgccg atttttgaga aatatcaagc gtggttttcc cgaatccggt 240
gttcgagaga aggaaac atg cac aac gac aac act ccc cac tcg cgt cgc      290

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Met His Asn Asp Asn Thr Pro His Ser Arg Arg

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5

10

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His Gly Asp Ala Ala Ala Ser Gly Ile Thr Arg Arg Gln Trp Leu Gln	
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Gly Ala Leu Ala Leu Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu	
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Arg Ala Leu Ala Asp Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met	
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Thr Leu Ser Glu Ser Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile	
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Gly Glu Arg Leu Leu Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala	
80 85 90	
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Gly Val Val Ser Asp Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys	
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Pro Gly Phe Trp Ala Asp Lys Pro Ile Glu Arg Gln Ala Met Ala	
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Ile Leu Leu Glu Ala Gly Pro Arg Met Pro Arg Trp Glu Ile Val Glu	
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Glu	Leu	Gly	Val	Trp	Gly	Pro	Gly	Pro	Glu	Glu	Asp	Leu	Tyr	Ser	Pro	
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cgc	aag	cag	ccg	tat	ccg	atg	ccg	ccg	ctg	ccg	ttg	tcg	ttc	aac	gag	1297
Arg	Lys	Gln	Pro	Tyr	Pro	Met	Pro	Pro	Leu	Pro	Leu	Ser	Phe	Asn	Glu	
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Thr Gly Val Ser Phe Tyr Ala Ser Glu Lys Leu Trp Pro Gly Arg Gly			
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Phe Asp Cys Phe His Glu Ile Leu Pro Gln Pro Glu Asn Arg Ile Val			
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Thr Tyr Ala Ile Asp Asp Tyr Val Lys Arg Gly Ala Ala His Thr Arg			
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gtc ggt acc gta aac gtg acg ctg acg atc gcc gcg ctc gcg ctg cgg			2353
Val Gly Thr Val Asn Val Thr Leu Thr Ile Ala Ala Leu Ala Leu Arg			
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 <212> PRT
 <213> Burkholderia cepacia

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 Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile Gly Glu Arg Leu Leu
 65 70 75 80
 Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala Asp Ser Leu Pro Gln
 85 90 95
 Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr Pro Glu Gln Glu Ser
 100 105 110
 Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu Gly Ile Val Asp Asn
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Tyr	Pro	Ser	Ser	Pro	Trp	Ala	Pro	His	Pro	Glu	Tyr	Gly	Pro	Pro	Asn
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Ser	Pro	Arg	Lys	Gln	Pro	Tyr	Pro	Met	Pro	Pro	Leu	Pro	Leu	Ser	Phe
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Glu	His	Arg	Val	Glu	Gly	Lys	Tyr	Phe	Val	Leu	Ala	Ala	Asn	Gly	Ile
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Glu	Thr	Pro	Lys	Ile	Leu	Leu	Met	Ser	Ala	Asn	Arg	Asp	Phe	Pro	Asn
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Gly	Val	Ala	Asn	Ser	Ser	Asp	Met	Val	Gly	Arg	Asn	Leu	Met	Asp	His
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Lys	Pro	Asp	Glu	Leu	Asp	Ala	Gln	Ile	Arg	Asp	Arg	Ser	Ala	Arg	Tyr				
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Glu	Ile	Thr	Tyr	Ala	Ile	Asp	Asp	Tyr	Val	Lys	Arg	Gly	Ala	Ala	His				
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<213> Burkholderia cepacia

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 Val Arg Lys Ser Thr Leu Thr Phe Leu Leu Ala Gly Cys
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 Leu Ala Leu Pro Gly Leu Ala Arg Ala Ala Asp Ser Ala Asp Pro Ala
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 Cys His Thr Ala Lys Gly Gly Lys Pro Phe Ala Gly Gly Leu Gly Met
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 Pro Val Pro Met Leu Gly Lys Ile Tyr Thr Ser Asn Ile Thr Pro Asp
 65 70 75
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 Pro Asp Thr Gly Ile Gly Asn Trp Thr Phe Glu Asp Phe Glu Arg Ala
 80 85 90
 gtg cgg cac ggc gta tgc aag aac ggc gac aac ctg tac ccg gcg atg 999
 Val Arg His Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met
 95 100 105
 ccg tac gtg tgc tac gcg aag atc aac gac gac gac gtg caa gcg ctg 1047
 Pro Tyr Val Ser Tyr Ala Lys Ile Asn Asp Asp Asp Val Gln Ala Leu
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 Tyr Ala Tyr Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro
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 aag aac gag atc ccc gcg ctg ctg agc atg cgc tgg ccg ctg aag atc 1143
 Lys Asn Glu Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile
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 Trp Asn Trp Leu Phe Leu Lys Asp Gly Val Tyr Gln Pro Lys Pro Glu
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 cag agc gcc gag tgg aac cgc ggc gcc tat ctc gtg cag ggc ctc gcg 1239
 Gln Ser Ala Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala
 175 180 185
 cac tgc agc acg tgc cac acg ccg cgc ggc atc gcg atg cag gag aag 1287
 His Cys Ser Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys
 190 195 200 205
 tgc ctc gac gaa acg ggc ggc agc ttc ctg tgc ggc tgc gtg ctc gcg 1335

Ser	Leu	Asp	Glu	Thr	Gly	Gly	Ser	Phe	Leu	Ser	Gly	Ser	Val	Leu	Ala	
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Gly	Trp	Asp	Gly	Tyr	Asn	Ile	Thr	Ser	Asp	Pro	Asn	Ala	Gly	Ile	Gly	
			225					230					235			
ggc	tgg	acg	cag	cag	cag	ctc	gtc	cag	tac	ctg	cgc	acc	ggc	agc	gtg	1431
Gly	Trp	Thr	Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	
			240					245					250			
ccg	ggc	ctc	gcg	cag	gcg	gcc	ggc	ccg	atg	gcc	gag	gcg	atc	gag	cac	1479
Pro	Gly	Leu	Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Ile	Glu	His	
			255				260					265				
agc	ttc	tcg	aag	atg	acc	gaa	gcc	gac	atc	ggc	ggc	ccg	atg	gcc	gag	1527
Ser	Phe	Ser	Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Gly	Pro	Met	Ala	Glu	
270						275				280					285	
gcg	atc	gag	cac	agc	ttc	tcg	aag	atg	acc	gaa	gcc	gac	atc	ggc	cgc	1575
Ala	Ile	Glu	His	Ser	Phe	Ser	Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Arg	
				290					295					300		
tcg	tcg	tgg	ggc	aag	ccg	gcc	gag	gat	ggc	ctg	aag	ctg	cgc	ggc	gtc	1623
Ser	Ser	Trp	Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	
			305					310					315			
gcg	ctc	gcg	tcg	tcg	ggc	atc	gat	ccg	gca	ccg	ctg	tat	ctc	ggc	aac	1671
Ala	Leu	Ala	Ser	Ser	Gly	Ile	Asp	Pro	Ala	Pro	Leu	Tyr	Leu	Gly	Asn	
			320				325					330				
tgc	gcg	acc	tgc	cac	cag	atg	cag	ggc	aag	ggc	acg	ccg	gac	ggt	tac	1719
Cys	Ala	Thr	Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	
			335				340				345					
tac	ccg	ccg	tig	ttc	cac	aac	tcg	acg	gtc	ggc	gcg	tcg	aat	ccg	acc	1767
Tyr	Pro	Pro	Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Thr	
350					355					360					365	
aac	ctc	gtg	cag	gtg	atc	ctg	aac	ggc	gtg	cag	cgc	aag	gcc	ggc	agc	1815
Asn	Leu	Val	Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ala	Gly	Ser	
				370				375					380			
gag	gac	gtc	ggg	atg	ccc	gcg	ttc	cgc	cac	gag	ctg	tcg	gat	gcg	cag	1863
Glu	Asp	Val	Gly	Met	Pro	Ala	Phe	Arg	His	Glu	Leu	Ser	Asp	Ala	Gln	
			385					390					395			
atc	gcc	gcg	ctg	acg	aac	tac	ctg	acg	ggg	cag	ttc	ggc	aat	ccg	gcc	1911
Ile	Ala	Ala	Leu	Thr	Asn	Tyr	Leu	Thr	Gly	Gln	Phe	Gly	Asn	Pro	Ala	
			400				405					410				

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aatccggatgc ggcacgcccg cgcacgtttt tcgttgatcg agacatgac accgaaccaa 2140
ccgtttctcgc cgtcccagcg cgaatgctcg ctgctgctgt cccgaatcct gctcgtgac 2200
ctgttcgtga tgttcggctg gaagaagatt atcgacttct ccggtacgat cgcgttcacg 2260
ggcagcgagg ggcgcgccggc gccgatcatt tcggcggcga tctccgtcgt gatggagctc 2320
atcgtcggga ttgcgatact cgtcggtttc cagacgcggc cgctcgcgct gtigtcttgcg 2380
ctgtacacga tcggtaccgg catcatcggc 2410

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<210> 12
 <211> 425
 <212> PRT
 <213> Burkholderia cepacia

<400> 12
 Val Arg Lys Ser Thr Leu Thr Phe Leu Leu Ala Gly Cys Leu Ala Leu
 1 5 10 15
 Pro Gly Leu Ala Arg Ala Ala Asp Ser Ala Asp Pro Ala His Val Lys
 20 25 30
 Arg Gly Glu Tyr Leu Ala Val Ala Gly Asp Cys Met Ala Cys His Thr
 35 40 45
 Ala Lys Gly Gly Lys Pro Phe Ala Gly Gly Leu Gly Met Pro Val Pro
 50 55 60
 Met Leu Gly Lys Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr
 65 70 75 80
 Gly Ile Gly Asn Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His
 85 90 95
 Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val
 100 105 110
 Ser Tyr Ala Lys Ile Asn Asp Asp Asp Val Gln Ala Leu Tyr Ala Tyr
 115 120 125
 Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu
 130 135 140
 Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp
 145 150 155 160
 Leu Phe Leu Lys Asp Gly Val Tyr Gln Pro Lys Pro Glu Gln Ser Ala
 165 170 175
 Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser
 180 185 190
 Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp
 195 200 205
 Glu Thr Gly Gly Ser Phe Leu Ser Gly Ser Val Leu Ala Gly Trp Asp
 210 215 220
 Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Gly Trp Thr
 225 230 235 240

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Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	Pro	Gly	Leu
				245					250					255	
Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Ile	Glu	His	Ser	Phe	Ser
			260					265					270		
Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Gly	Pro	Met	Ala	Glu	Ala	Ile	Glu
		275					280					285			
His	Ser	Phe	Ser	Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Arg	Ser	Ser	Trp
	290					295					300				
Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	Ala	Leu	Ala
305					310					315					320
Ser	Ser	Gly	Ile	Asp	Pro	Ala	Pro	Leu	Tyr	Leu	Gly	Asn	Cys	Ala	Thr
				325					330					335	
Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	Tyr	Pro	Pro
			340					345					350		
Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Thr	Asn	Leu	Val
		355					360					365			
Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ala	Gly	Ser	Glu	Asp	Val
	370					375					380				
Gly	Met	Pro	Ala	Phe	Arg	His	Glu	Leu	Ser	Asp	Ala	Gln	Ile	Ala	Ala
385					390					395					400
Leu	Thr	Asn	Tyr	Leu	Thr	Gly	Gln	Phe	Gly	Asn	Pro	Ala	Ala	Lys	Val
				405					410					415	
Thr	Glu	Gln	Asp	Val	Ala	Lys	Leu	Arg							
			420					425							

<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 13

tgcaccgtgc ggaaatctac tctcact

27

<210> 14

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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<400> 14

acttccitct tcagcgtgtc cgacatc

27

<210> 15

<211> 1441

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (121)..(1398)

<400> 15

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gctgacgata gccgcgctcg cgctgcggat gtcggacacg ctgaagaagg aagtcgtgac 120
gtg cgg aaa tct act ctc act ttc ctc atc gcc ggc tgc ctc gcg ttg 168
Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu
      1           5           10           15
ccg ggc ttc gcg cgc gcg gcc gat gcg gcc gat ccg gcg ctg gtc aag 216
Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys
           20           25           30
cgc ggc gaa tac ctc gcg acc gcc atg ccg gta ccg atg ctc ggc aag 264
Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys
           35           40           45
atc tac acg agc aac atc acg ccc gat ccc gat acg ggc gac tgc atg 312
Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met
           50           55           60
gcc tgc cac acc gtg aag ggc ggc aag ccg tac gcg ggc ggc ctt ggc 360
Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly
           65           70           75           80
ggc atc ggc aaa tgg acg ttc gag gac ttc gag cgc gcg gtg cgg cac 408
Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His
           85           90           95
ggc gtg tcg aag aac ggc gac aac ctg tat ccg gcg atg ccg tac gtg 456
Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val
           100           105           110
tcg tac gcg aag atc aag gac gac gac gta cgc gcg ctg tac gcc tac 504
Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr
           115           120           125
ttc atg cac ggc gtc gag ccg gtc aag cag gcg ccg ccg aag aac gag 552
Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu
           130           135           140

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atc cca gcg ctg cta agc atg cgc tgg ccg ctg aag atc tgg aac tgg	600
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp	
145 150 155 160	
ctg ttc ctg aag gac ggc ccg tac cag ccg aag ccg tcg cag agc gcc	648
Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala	
165 170 175	
gaa tgg aat cgc ggc gcg tat ctg gtg cag ggt ctc gcg cac tgc agc	696
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser	
180 185 190	
acg tgc cac acg ccg cgc ggc atc gcg atg cag gag aag tcg ctc gac	744
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp	
195 200 205	
gaa acc ggc ggc agc ttc ctc gcg ggg tcg gtg ctc gcc ggc tgg gac	792
Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp	
210 215 220	
ggc tac aac atc acg tcg gac ccg aat gcg ggg atc ggc agc tgg acg	840
Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr	
225 230 235 240	
cag cag cag ctc gtg cag tat ttg cgc acc ggc agc gtg ccg ggc gtc	888
Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Val	
245 250 255	
gcg cag gcg gcc ggg ccg atg gcc gag gcg gtc gag cac agc ttc tcg	936
Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Val Glu His Ser Phe Ser	
260 265 270	
aag atg acc gaa gcg gac atc ggt gcg atc gcc acg tac gtc cgc acg	984
Lys Met Thr Glu Ala Asp Ile Gly Ala Ile Ala Thr Tyr Val Arg Thr	
275 280 285	
gtg ccg gcc gtt gcc gac agc aac gcg aag cag ccg cgg tcg tcg tgg	1032
Val Pro Ala Val Ala Asp Ser Asn Ala Lys Gln Pro Arg Ser Ser Trp	
290 295 300	
ggc aag ccg gcc gag gac ggg ctg aag ctg cgc ggt gtc gcg ctc gcg	1080
Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala	
305 310 315 320	
tcg tcg ggc atc gat ccg gcg cgg ctg tat ctc ggc aac tgc gcg acg	1128
Ser Ser Gly Ile Asp Pro Ala Arg Leu Tyr Leu Gly Asn Cys Ala Thr	
325 330 335	
tgc cac cag atg cag ggc aag ggc acg ccg gac ggc tat tac ccg tcg	1176
Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Ser	
340 345 350	
ctg ttc cac aac tcc acc gtc ggc gcg tcg aat ccg tcg aac ctc gtg	1224
Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Ser Asn Leu Val	
355 360 365	
cag gtg atc ctg aac ggc gtg cag cgc aag atc ggc agc gag gat atc	1272

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Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ile Gly Ser Glu Asp Ile
 370 375 380
 ggg atg ccc gct ttc cgc tac gat ctg aac gac gcg cag atc gcc gcg 1320
 Gly Met Pro Ala Phe Arg Tyr Asp Leu Asn Asp Ala Gln Ile Ala Ala
 385 390 395 400
 ctg acg aac tac gtg acc gcg cag ttc ggc aat ccg gcg gcg aag gtg 1368
 Leu Thr Asn Tyr Val Thr Ala Gln Phe Gly Asn Pro Ala Ala Lys Val
 405 410 415
 acg gag cag gac gtc gcg aag ctg cgc tga catagtcggg cgcgccgaca 1418
 Thr Glu Gln Asp Val Ala Lys Leu Arg
 420 425
 cggcgcaacc gataggacag gag 1441

<210> 16

<211> 425

<212> PRT

<213> Burkholderia cepacia

<400> 16

Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu
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 Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys
 20 25 30
 Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys
 35 40 45
 Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met
 50 55 60
 Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly
 65 70 75 80
 Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His
 85 90 95
 Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val
 100 105 110
 Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr
 115 120 125
 Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu
 130 135 140
 Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp
 145 150 155 160
 Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala
 165 170 175
 Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser
 180 185 190

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Thr	Cys	His	Thr	Pro	Arg	Gly	Ile	Ala	Met	Gln	Glu	Lys	Ser	Leu	Asp
		195					200					205			
Glu	Thr	Gly	Gly	Ser	Phe	Leu	Ala	Gly	Ser	Val	Leu	Ala	Gly	Trp	Asp
	210					215					220				
Gly	Tyr	Asn	Ile	Thr	Ser	Asp	Pro	Asn	Ala	Gly	Ile	Gly	Ser	Trp	Thr
225					230					235					240
Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	Pro	Gly	Val
				245					250					255	
Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Val	Glu	His	Ser	Phe	Ser
			260					265					270		
Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Ala	Ile	Ala	Thr	Tyr	Val	Arg	Thr
		275					280					285			
Val	Pro	Ala	Val	Ala	Asp	Ser	Asn	Ala	Lys	Gln	Pro	Arg	Ser	Ser	Trp
	290					295					300				
Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	Ala	Leu	Ala
305					310					315					320
Ser	Ser	Gly	Ile	Asp	Pro	Ala	Arg	Leu	Tyr	Leu	Gly	Asn	Cys	Ala	Thr
				325					330					335	
Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	Tyr	Pro	Ser
			340					345						350	
Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Ser	Asn	Leu	Val
		355					360					365			
Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ile	Gly	Ser	Glu	Asp	Ile
	370					375					380				
Gly	Met	Pro	Ala	Phe	Arg	Tyr	Asp	Leu	Asn	Asp	Ala	Gln	Ile	Ala	Ala
385					390					395					400
Leu	Thr	Asn	Tyr	Val	Thr	Ala	Gln	Phe	Gly	Asn	Pro	Ala	Ala	Lys	Val
				405					410					415	
Thr	Glu	Gln	Asp	Val	Ala	Lys	Leu	Arg							
			420					425							

<210> 17

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: heme binding motif

<220>

<221> UNSURE

<222> (2, 3)

<223> Xaa=unknown

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<400> 17

Cys Xaa Xaa Cys His

1

5

<210> 18

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 18

catgccatgg cacacaacga caacact

27

<210> 19

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 19

cccaagcttg ggtcagactt ccttcttcag c

31